

SEQUENCE LISTING

<110> Moloney, Maurice
Boothe, Joseph
Rooijen, Gijs Van

<120> Oil Bodies and Associated Proteins as Affinity Matrices

<130> 9369-161

<140> US 09/707,167

<141> 2000-11-07

<150> US 09/319,275

<151> 1999-08-27

<160> 14

B² <170> PatentIn version 3.1

<210> 1

<211> 522

<212> DNA

<213> Arabidopsis Thaliana

<220>

<221> CDS

<222> (1)..(522)

<223>

<400> 1
atg gcg gat aca gct aga gga acc cat cac gat atc atc ggc aga gac 48
Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp
1 5 10 15
cag tac ccg atg atg ggc cga gac cga gac cag tac cag atg tcc gga 96
Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
20 25 30
cga gga tct gac tac tcc aag tct agg cag att gct aaa gct gca act 144
Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
35 40 45

gct gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc ctt	192
Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu	
50 55 60	
ggt gga act gtc ata gct ttg act gtt gca aca cct ctg ctc gtt atc	240
Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile	
65 70 75 80	
ttc agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc ctc atc	288
Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile	
85 90 95	
acc ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata acc gtt	336
Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val	
100 105 110	
ttc tct tgg att tac aag tac gca acg gga gag cac cca cag gga tca	384
Phe Ser Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser	
115 120 125	
gac aag ttg gac agt gca agg atg aag ttg gga agc aaa gct cag gat	432
Asp Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp	
130 135 140	
ctg aaa gac aga gct cag tac tac gga cag caa cat act ggt ggg gaa	480
Leu Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu	
145 150 155 160	
cat gac cgt gac cgt act cgt ggt ggc cag cac act act taa	522
His Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr	
165 170	

<210> 2

<211> 173

<212> PRT

<213> Arabidopsis Thaliana

<400> 2

Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp	
1 5 10 15	
Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly	
20 25 30	
Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr	
35 40 45	
Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu	
50 55 60	
Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile	
65 70 75 80	
Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile	
85 90 95	
Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val	

100 105 110

Phe Ser Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser
115 120 125

Asp Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp
130 135 140

Leu Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu
145 150 155 160

His Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr
165 170

<210> 3
<211> 2115
<212> DNA
<213> Artificial Sequence

<220>
<223> Oleosin - Hirudin Fusion
<220>
<221> CDS
<222> (862)..(1215)
<223>

<220>
<221> CDS
<222> (1456)..(1833)
<223>

<400> 3
ctatacccaa cctcggtctt ggtcacacca ggaactctct ggtaagctag ctccactccc 60
cagaaacaac cggcgccaaa ttgccggaat tgctgacctg aagacggaac atcatcgctg 120
ggtccttggg cgattgcggc ggaagatggg tcagcttggg cttgaggacg agacccgaat 180
cgagtctgtt gaaaggttgt tcattgggat ttgtatacgg agattggctg tcgagagggtt 240
tgaggggaaag gacaaatggg tttggctctg gagaaagaga gtgcggcttt agagagagaa 300
ttgagagggtt tagagagaga tgcggcggcg atgacgggag gagagacgac gaggacctgc 360
attatcaaag cagtgcctg gtgaaatttg gaacttttaa gaggcagata gatttattat 420
ttgtatccat tttcttcatt gttctagaat gtcgcggaac aaattttaaa actaaatcct 480
aaatttttct aattttgttg ccaatagtgg atatgtgggc cgtatagaag gaatctattg 540

aaggcccaaa cccatactga cgagcccaaa ggttcgtttt gcgttttatg tttcggttcg	600
atgccaacgc cacattctga gctaggcaaa aaacaaacgt gtctttgaat agactcctct	660
cgttaacaca tgcagcggct gcatgggtgac gccattaaca cgtggcctac aattgcatga	720
tgtctccatt gacacgtgac ttctcgtctc ctttcttaat atatctaaca aacactccta	780
cctcttccaa aatatataca catcttttttg atcaatctct cattcaaaat ctcatctct	840
ctagtaacaa agaacaaaaa a atg gcg gat aca gct aga gga acc cat cac	891
Met Ala Asp Thr Ala Arg Gly Thr His	1 5 10
gat atc atc ggc aga gac cag tac ccg atg atg ggc cga gac cga gac	939
Asp Ile Ile Gly Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg Asp	15 20 25
cag tac cag atg tcc gga cga gga tct gac tac tcc aag tct agg cag	987
Gln Tyr Gln Met Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln	30 35 40
att gct aaa gct gca act gct gtc aca gct ggt ggt tcc ctc ctt gtt	1035
Ile Ala Lys Ala Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu Val	45 50 55
ctc tcc agc ctt acc ctt gtt gga act gtc ata gct ttg act gtt gca	1083
Leu Ser Ser Leu Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val Ala	60 65 70
aca cct ctg ctc gtt atc ttc agc cca atc ctt gtc ccg gct ctc atc	1131
Thr Pro Leu Leu Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu Ile	75 80 85 90
aca gtt gca ctc ctc atc acc ggt ttt ctt tcc tct gga ggg ttt ggc	1179
Thr Val Ala Leu Leu Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly	95 100 105
att gcc gct ata acc gtt ttc tct tgg att tac aag taagcacaca	1225
Ile Ala Ala Ile Thr Val Phe Ser Trp Ile Tyr Lys	110 115
tttatcatct tacttcataa ttttgtgcaa tatgtgcatg catgtgttga gccagtagct	1285
ttggatcaat ttttttggtc gaataacaaa tgtaacaata agaaattgca aattctaggg	1345
aacatttggt taactaaata cgaaatttga cctagctagc ttgaatgtgt ctgtgtatat	1405
catctatata ggtaaaatgc ttggtatgat acctattgat tgtgaatagg tac gca	1461
Tyr Ala	120
acg gga gag cac cca cag gga tca gac aag ttg gac agt gca agg atg	1509
Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala Arg Met	125 130 135
aag ttg gga agc aaa gct cag gat ctg aaa gac aga gct cag tac tac	1557
Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr	140 145 150
gga cag caa cat act ggt tgg gaa cat gac cgt gac cgt act cgt ggt	1605
Gly Gln Gln His Thr Gly Trp Glu His Asp Arg Asp Arg Thr Arg Gly	155 160 165
ggc cag cac act act gcg atc gaa ggg aga atc act tac act gac tgt	1653
Gly Gln His Thr Thr Ala Ile Glu Gly Arg Ile Thr Tyr Thr Asp Cys	170 175 180
act gaa tct gga cag aac ctc tgt ctc tgt gaa gga tct aac gtt tgt	1701
Thr Glu Ser Gly Gln Asn Leu Cys Leu Cys Glu Gly Ser Asn Val Cys	

185 190 195 200

gga aag gga aac aag tgt atc ctc gga tct aac gga aag gga aac cag 1749
Gly Lys Gly Asn Lys Cys Ile Leu Gly Ser Asn Gly Lys Gly Asn Gln
 205 210 215

tgt gtt act gga gaa gga act cca aac cca gaa tct cac aac aac gga 1797
Cys Val Thr Gly Glu Gly Thr Pro Asn Pro Glu Ser His Asn Asn Gly
 220 225 230

gac ttc gaa gaa atc cct gaa gaa tac ctc cag taa gtcgactcta 1843
Asp Phe Glu Glu Ile Pro Glu Glu Tyr Leu Gln
 235 240

gacggatctc cccgatcggtc aaacatttgg caataaagtt tcttaagatt gaatcctggt 1903

gccgggtcttg cgatgattat catataattt ctgttgaatt acgttaagca tgtaataatt 1963

aacatgtaat gcatgacggt atttatgaga tgggttttta tgattagagt cccgcaatta 2023

tacattttaat acgcataga aaacaaaata tagcgcgcaa actaggataa attatcgcgc 2083

gcggtgtcat ctatgttact agatcggaat tc 2115

<210> 4

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> Oleosin - Hirudin Fusion

<400> 4

Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp
1 5 10 15

Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
 20 25 30

Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
 35 40 45

Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
50 55 60

Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
65 70 75 80

Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
 85 90 95

Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
 100 105 110

Phe Ser Trp Ile Tyr Lys
 115

<210> 5
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Oleosin - Hirudin Fusion
<400> 5

Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
1 5 10 15

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Trp Glu His Asp Arg Asp Arg Thr
35 40 45

Arg Gly Gly Gln His Thr Thr Ala Ile Glu Gly Arg Ile Thr Tyr Thr
50 55 60

Asp Cys Thr Glu Ser Gly Gln Asn Leu Cys Leu Cys Glu Gly Ser Asn
65 70 75 80

Val Cys Gly Lys Gly Asn Lys Cys Ile Leu Gly Ser Asn Gly Lys Gly
85 90 95

Asn Gln Cys Val Thr Gly Glu Gly Thr Pro Asn Pro Glu Ser His Asn
100 105 110

Asn Gly Asp Phe Glu Glu Ile Pro Glu Glu Tyr Leu Gln
115 120 125

<210> 6
<211> 2366
<212> DNA
<213> Artificial Sequence

<220>
<223> Oleosin - Metallothionein Fusion
<220>
<221> CDS
<222> (1092)..(1856)
<223>

```

<400> 6
gagctcaaat acgatctgat actgataacg tctagatttt tagggttaaa gcaatcaatc 60
acctgacgat tcaaggtggt tggatcatga cgattccaga aaacatcaag caagctctca 120
aagctacact ctttgggatac atactgaact ctaacaacct cgttatgtcc cgtagtgcca 180
gtacagacat cctcgttaact cggattatgc acgatgccat ggctataccc aacctcggtc 240
ttggtcacac caggaactct ctggtaagct agctccactc cccagaaaca accggcgcca 300
aattgccgga attgctgacc tgaagacgga acatcatcgt cgggtccttg ggcgattgcg 360
gcggaagatg ggtcagcttg ggcttgagga cgagaccoga atcgagtctg ttgaaaggtt 420
gttcattggg atttgtatac ggagattggg cgtcgagagg tttgagggaa aggacaaatg 480
ggtttggtc tggagaaaga gagtggcggt ttagagagag aattgagagg tttagagaga 540
gatgcggcgg cgatgacggg aggagagacg acgaggacct gcattatcaa agcagtgcg 600
tggtgaaatt tggaaactttt aagaggcaga tagatttatt atttgtatcc attttcttca 660
ttgttctaga atgtcgcgga acaaatttta aaactaaatc ctaaattttt ctaattttgt 720
tgccaatagt ggatatgtgg gccgtataga aggaatctat tgaaggccca aaccataact 780
gacgagccca aagggttcgtt ttgcgtttta tgtttcggtt cgatgccaac gccacattct 840
gagctaggca aaaaacaaac gtgtctttga atagactcct ctcgttaaca catgcagcgg 900
ctgcatgggtg acgccattaa cacgtggcct acaattgcat gatgtctcca ttgacacgtg 960
acttctcgtc tcctttctta atatatctaa caaacactcc tacctcttcc aaaatatata 1020
cacatctttt tgatcaatct ctcatc aaa atctcattct ctctagtaaa caggatcccc 1080
ctcgcggccg c atg gcg gat aca gct aga acc cat cac gat gtc aca agt 1130
          1      5      10
          Met Ala Asp Thr Ala Arg Thr His His Asp Val Thr Ser

cga gat cag tat ccc cga gac cga gac cag tat tct atg atc ggt cga 1178
Arg Asp Gln Tyr Pro Arg Asp Arg Asp Gln Tyr Ser Met Ile Gly Arg
          15      20      25

gac cgt gac cag tac tct atg atg ggc cga gac cga gac cag tac aac 1226
Asp Arg Asp Gln Tyr 35 Ser Met Met Gly Arg Asp Arg Asp Gln Tyr Asn 45
          30      35      40      45

atg tat ggt cga gac tac tcc aag tct aga cag att gct aag gct gtt 1274
Met Tyr Gly Arg Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Val 60
          50      55      60

acc gca gtc acg gcg ggt ggg tcc ctc ctt gtc ctc tcc agt ctc acc 1322
Thr Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr 75
          65      70      75

ctt gtt ggt act gtc att gct ttg act gtt gcc act cca ctc ctc gtt 1370
Leu Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val 90
          80      85      90

atc ttt agc cca atc ctc gtg ccg gct ctc atc acc gta gca ctt ctc 1418
Ile Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu 105
          95      100      105

atc act ggc ttt ctc tcc tct ggt ggg ttt gcc att gca gct ata acc 1466
Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe Ala Ile Ala Ala Ile Thr 125
          110      115      120

```

gtc ttc tcc tgg atc tat aag tac gca acg gga gag cac cca cag ggg	1514
Val Phe Ser Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly	
130 135 140	
tca gat aag ttg gac agt gca agg atg aag ctg gga acc aaa gct cag	1562
Ser Asp Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Thr Lys Ala Gln	
145 150 155	
gat att aaa gac aga gct caa tac tac gga cag caa cat aca ggt ggt	1610
Asp Ile Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly	
160 165 170	
gag cat gac cgt gac cgt act cgt ggt ggc cag cac act act ctc gtt	1658
Glu His Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Leu Val	
175 180 185	
cca cga gga tcc atg gat ccc aac tgc tcc tgt gcc gcc agt gac tcc	1706
Pro Arg Gly Ser Met Asp Pro Asn Cys Ser Cys Ala Ala Ser Asp Ser	
190 195 200 205	
tgc acc tgc gcc ggc tcc tgc aag tgc aaa gag tgc aaa tgc acc tcc	1754
Cys Thr Cys Ala Gly Ser Cys Lys Cys Lys Glu Cys Lys Cys Thr Ser	
210 215 220	
tgc aag aaa agc tgc tgc tcc tgc tgt cct gtg ggc tgt gcc aag tgt	1802
Cys Lys Lys Ser Cys Cys Ser Cys Cys Pro Val Gly Cys Ala Lys Cys	
225 230 235	
gcc cag ggc tgc atc tgc aaa ggg gcg tgc gac aag tgc agc tgc tgt	1850
Ala Gln Gly Cys Ile Cys Lys Gly Ala Ser Asp Lys Cys Ser Cys Cys	
240 245 250	
gcc tga gcggccgcga gggctgcaga atgagttcca agatggtttg tgacgaagtt	1906
Ala	
agttggttgt ttttatggaa ctttgtttaa gcttgtaatg tggaaagaac gtgtggcttt	1966
gtggttttta aatgttggtg aataaagatg tttcctttgg attaaactagt atttttccta	2026
ttggttttcat ggtttttagca cacaacattt taaatatgct gttagatgat atgctgcctg	2086
ctttattatt tacttaccoc tcaccttcag tttcaaagtt gttgcaatga ctctgtgtag	2146
tttaagatcg agtgaaagta gattttgtct atattttatta ggggtatttg atatgcta	2206
ggtaaacatg gtttatgaca gcgtactttt ttggttatgg tgttgacgtt tccttttaaa	2266
cattatagta gcgtccttgg tctgtgttca ttggttgaac aaaggcacac tcacttgag	2326
atgccgtctc cactgatatt tgaacaaaga attcgggtacc	2366
<210> 7	
<211> 254	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Oleosin - Metallothionein Fusion	
<400> 7	
Met Ala Asp Thr Ala Arg Thr His His Asp Val Thr Ser Arg Asp Gln	

1	5	10	15
Tyr	Pro	Arg	Asp
	20	Arg	Asp
Gln	Tyr	Ser	Met
	25	Ile	Gly
Arg	Asp	Arg	Asp
	30	Arg	Asp
Gln	Tyr	Ser	Met
	35	Met	Gly
Arg	Asp	Arg	Asp
	40	Gln	Tyr
Asn	Met	Tyr	Gly
	45		
Arg	Asp	Tyr	Ser
	50	Lys	Ser
Arg	Gln	Ile	Ala
	55	Lys	Ala
Val	Thr	Ala	Val
	60		
Thr	Ala	Gly	Gly
	65	Ser	Leu
Leu	Val	Leu	Ser
	70	Ser	Leu
Thr	Leu	Val	Gly
	75		80
Thr	Val	Ile	Ala
	85	Leu	Thr
Val	Ala	Thr	Pro
	90	Leu	Leu
Val	Ile	Phe	Ser
	95		
Pro	Ile	Leu	Val
	100	Pro	Ala
Leu	Ile	Thr	Val
	105	Ala	Leu
Leu	Ile	Thr	Gly
	110		
Phe	Leu	Ser	Ser
	115	Gly	Gly
Phe	Ala	Ile	Ala
	120	Ala	Ile
Thr	Val	Phe	Ser
	125		
Trp	Ile	Tyr	Lys
	130	Tyr	Ala
Thr	Gly	Glu	His
	135	Pro	Gln
Gly	Ser	Asp	Lys
	140		
Leu	Asp	Ser	Ala
	145	Arg	Met
Lys	Leu	Gly	Thr
	150	Lys	Ala
Gln	Asp	Ile	Lys
	155		160
Asp	Arg	Ala	Gln
	165	Tyr	Tyr
Gly	Gln	Gln	His
	170	Thr	Gly
Gly	Glu	His	Asp
	175		
Arg	Asp	Arg	Thr
	180	Arg	Gly
Gly	Gln	His	Thr
	185	Thr	Thr
Leu	Val	Pro	Arg
	190		
Ser	Met	Asp	Pro
	195	Asn	Cys
Ser	Cys	Ala	Ala
	200	Ser	Asp
Ser	Cys	Thr	Cys
	205		
Ala	Gly	Ser	Cys
	210	Lys	Cys
Lys	Cys	Lys	Glu
	215	Cys	Cys
Thr	Ser	Cys	Lys
	220		
Ser	Cys	Cys	Ser
	225	Cys	Cys
Pro	Val	Gly	Cys
	230	Ala	Lys
Cys	Ala	Gln	Gly
	235		240
Cys	Ile	Cys	Lys
	245	Gly	Ala
Ser	Asp	Lys	Cys
	250	Ser	Cys
Cys	Cys	Ala	

<210> 8

<211> 804

<212> DNA

<213> Artificial Sequence

<220>

<223> Protein A Primers

<220>

<221> CDS

<222> (5)..(796)

<223>

```
<400> 8
ctcc atg gat caa cgc aat ggt ttt atc caa agc ctt aaa gat gat cca 49
      Met Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro
      1          5          10          15

agc caa agt gct aac gtt tta ggt gaa gct caa aaa ctt aat gac tct 97
Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys Leu Asn Asp Ser
      20          25          30

caa gct cca aaa gct gat gcg caa caa aat aac ttc aac aaa gat caa 145
Gln Ala Pro Lys Ala Asp Ala Gln Gln Asn Asn Phe Asn Lys Asp Gln
      35          40          45

caa agc gcc ttc tat gaa atc ttg aac atg cct aac tta aac gaa gcg 193
Gln Ser Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Ala
      50          55          60

caa cgt aac ggc ttc att caa agt ctt aaa gac gac cca agc caa agc 241
Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser
      65          70          75

act aac gtt tta ggt gaa gct aaa aaa tta aac gaa tct caa gca ccg 289
Thr Asn Val Leu Gly Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro
      80          85          90          95

aaa gct gat aac aat ttc aac aaa gaa caa caa aat gct ttc tat gaa 337
Lys Ala Asp Asn Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu
      100          105          110

atc ttg aat atg cct aac tta aac gaa gaa caa cgc aat ggt ttc atc 385
Ile Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile
      115          120          125

caa agc tta aaa gat gac cca agc caa agt gct aac cta ttg tca gaa 433
Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ser Glu
      130          135          140

gct aaa aag tta aat gaa tct caa gca ccg aaa gcg gat aac aaa ttc 481
Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Lys Phe
      145          150          155

aac aaa gaa caa caa aat gct ttc tat gaa atc tta cat tta cct aac 529
Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn
      160          165          170          175

tta aac gaa gaa caa cgc aat ggt ttc atc caa agc cta aaa gat gac 577
Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp
      180          185          190

cca agc caa agc gct aac ctt tta gca gaa gct aaa aag cta aat gat 625
Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp
      195          200          205

gct caa gca cca aaa gct gac aac aaa ttc aac aaa gaa caa caa aat 673
Ala Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn
```

210	215	220	
gct ttc tat gaa att tta cat tta cct aac tta act gaa gaa caa cgt			721
Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg			
225	230	235	
aac ggc ttc atc caa agc ctt aaa gac gat ccg ggg aat tcc cgg gga			769
Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Gly Asn Ser Arg Gly			
240	245	250	255
tcc gtc gac ctg cag ata aca aat tag aagcttgc			804
Ser Val Asp Leu Gln Ile Thr Asn			
260			

<210> 9

<211> 263

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein A Primers

<400> 9

Met Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
1 5 10 15

Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys Leu Asn Asp Ser Gln
20 25 30

Ala Pro Lys Ala Asp Ala Gln Gln Asn Asn Phe Asn Lys Asp Gln Gln
35 40 45

Ser Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Ala Gln
50 55 60

Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Thr
65 70 75 80

Asn Val Leu Gly Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys
85 90 95

Ala Asp Asn Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile
100 105 110

Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln
115 120 125

Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ser Glu Ala
130 135 140

Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn
145 150 155 160

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
165 170 175

Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro
180 185 190

Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
195 200 205

Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala
210 215 220

Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn
225 230 235 240

Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Gly Asn Ser Arg Gly Ser
245 250 255

Val Asp Leu Gln Ile Thr Asn
260

<210> 10

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer Bk 266

<400> 10
tccatggatc aacgcaatgg tttatc

26

<210> 11

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer Bk 267

<400> 11
gcaagcttct aatttggtat ctgcaggtc

29

<210> 12

<211> 2709

<212> DNA

<213> Artificial Sequence

<220>

<223> Oleosin - Protein A Fusion

<220>

<221> CDS

<222> (868)..(1218)

<223>

<220>

<221> CDS

<222> (1462)..(2433)

<223>

<400> 12
ccatggctat acccaacctc ggtcttggtc acaccaggaa ctctctggta agctagctcc 60
actccccaga aacaaccggc gccaaattgc cggaattgct gacctgaaga cggaacatca 120
tcgtcgggtc cttgggcgat tgcggcggaa gatgggtcag cttgggcttg aggacgagac 180
ccgaatcgag tctgttgaaa ggttggtcat tgggatttgt atacggagat tggtcgtcga 240
gagggtttgag ggaaaggaca aatgggtttg gctctggaga aagagagtgc ggctttagag 300
agagaattga gaggtttaga gagagatgcg gcggcgatga cgggaggaga gacgacgagg 360
acctgcatta tcaaagcagt gacgtggtga aatttggaac ttttaagagg cagatagatt 420
tattatttgt atccattttc ttcatgttgc tagaatgtcg cggaacaaat tttaaaacta 480
aatcctaaat ttttctaatt ttgttgccaa tagtggatat gtgggccgta tagaaggaat 540
ctattgaagg cccaaacca tactgacgag cccaaagggt cgttttgctg tttatgtttc 600
ggttcgatgc caacgccaca ttctgagcta ggcaaaaaac aaacgtgtct ttgaatagac 660
tctctcgtt aacacatgca gcggctgcat ggtgacgcca ttaacacgtg gcctacaatt 720
gcatgatgtc tccattgaca cgtgacttct cgtctccttt cttaatatat ctaacaaaca 780
ctctacctc ttccaaaata tatacacatc tttttgatca atctctcatt caaaatctca 840
ttctctctag taaacaagaa caaaaaa atg gcg gat aca gct aga gga acc cat 894
Met Ala Asp Thr Ala Arg Gly Thr His
1 5
cac gat atc atc ggc aga gac cag tac ccg atg atg ggc cga gac cga 942
His Asp Ile Ile Gly Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg
10 15 20 25
gac cag tac cag atg tcc gga cga gga tct gac tac tcc aag tct agg 990
Asp Gln Tyr Gln Met Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg
30 35 40
cag att gct aaa gct gca act gct gtc aca gct ggt ggt tcc ctc ctt 1038
Gln Ile Ala Lys Ala Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu

45	50	55	
gtt ctc tcc agc ctt acc ctt gtt gga act gtc ata gct ttg act gtt Val Leu Ser Ser Leu Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val 60 65 70			1086
gca aca cct ctg ctc gtt atc ttc agc cca atc ctt gtc ccg gct ctc Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu 75 80 85			1134
atc aca gtt gca ctc ctc atc acc ggt ttt ctt tcc tct gga ggg ttt Ile Thr Val Ala Leu Leu Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe 90 95 100 105			1182
ggc att gcc gct ata acc gtt ttc tct tgg att tac aagtaagcac Gly Ile Ala Ala Ile Thr Val Phe Ser Trp Ile Tyr 110 115			1228
acatttatca tcttacttca taattttgtg caatatgtgc atgcatgtgt tgagccagta			1288
gctttggatc aatttttttg gtcgaataac aaatgtaaca ataagaaatt gcaaattcta			1348
gggaacattt ggtaactaa atacgaaatt tgacctagct agcttgaatg tgtctgtgta			1408
tatcatctat ataggtaaaaa tgcttggtat gatacctatt gattgtgaat agg tac Tyr			1464
gca acg gga gag cac cca cag gga tca gac aag ttg gac agt gca agg Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala Arg 120 125 130			1512
atg aag ttg gga agc aaa gct cag gat ctg aaa gac aga gct cag tac Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln Tyr 135 140 145 150			1560
tac gga cag caa cat act ggt ggg gaa cat gac cgt gac cgt act cgt Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr Arg 155 160 165			1608
ggt ggc cag cac act act ctc gtt cca cga gga tcc atg gat caa cgc Gly Gly Gln His Thr Thr Leu Val Pro Arg Gly Ser Met Asp Gln Arg 170 175 180			1656
aat ggt ttt atc caa agc ctt aaa gat gat cca agc caa agt gct aac Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn 185 190 195			1704
gtt tta ggt gaa gct caa aaa ctt aat gac tct caa gct cca aaa gct Val Leu Gly Glu Ala Gln Lys Leu Asn Asp Ser Gln Ala Pro Lys Ala 200 205 210			1752
gat gcg caa caa aat aac ttc aac aaa gat caa caa agc gcc ttc tat Asp Ala Gln Gln Asn Asn Phe Asn Lys Asp Gln Gln Ser Ala Phe Tyr 215 220 225 230			1800
gaa atc ttg aac atg cct aac tta aac gaa gcg caa cgt aac ggc ttc Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly Phe 235 240 245			1848
att caa agt ctt aaa gac gac cca agc caa agc act aac gtt tta ggt Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Thr Asn Val Leu Gly 250 255 260			1896
gaa gct aaa aaa tta aac gaa tct caa gca ccg aaa gct gat aac aat Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Asn 265 270 275			1944
ttc aac aaa gaa caa caa aat gct ttc tat gaa atc ttg aat atg cct Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met Pro 280 285 290			1992

aac tta aac gaa gaa caa cgc aat ggt ttc atc caa agc tta aaa gat 2040
Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp
295 300 305 310

gac cca agc caa agt gct aac cta ttg tca gaa gct aaa aag tta aat 2088
Asp Pro Ser Gln Ser Ala Asn Leu Leu Ser Glu Ala Lys Lys Leu Asn
315 320 325

gaa tct caa gca ccg aaa gcg gat aac aaa ttc aac aaa gaa caa caa 2136
Glu Ser Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln
330 335 340

aat gct ttc tat gaa atc tta cat tta cct aac tta aac gaa gaa caa 2184
Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu Gln
345 350 355

cgc aat ggt ttc atc caa agc cta aaa gat gac cca agc caa agc gct 2232
Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala
360 365 370

aac ctt tta gca gaa gct aaa aag cta aat gat gct caa gca cca aaa 2280
Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys
375 380 385 390

gct gac aac aaa ttc aac aaa gaa caa caa aat gct ttc tat gaa att 2328
Ala Asp Asn Lys Phe Asn Lys Glu Gln Asn Ala Phe Tyr Glu Ile
395 400 405

tta cat tta cct aac tta act gaa gaa caa cgt aac ggc ttc atc caa 2376
Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln
410 415 420

agc ctt aaa gac gat ccg ggg aat tcc cgg gga tcc gtc gac ctg cag 2424
Ser Leu Lys Asp Asp Pro Gly Asn Ser Arg Gly Ser Val Asp Leu Gln
425 430 435

ata aca aat tagaagcttg catgcctgca ggtcgatcgt tcaaacattt 2473
Ile Thr Asn
440

ggcaataaag tttcttaaga ttgaatcctg ttgccggtct tgcatgatt atcatataat 2533

ttctgttgaa ttacgttaag catgtaataa ttaacatgta atgcatgacg ttatttatga 2593

gatgggtttt tatgattaga gtcccgaat tatacattta atacgcgata gaaaacaaaa 2653

tatagcgcgc aaactaggat aaattatcgc gcgcggtgtc atctatgtta ctagat 2709

<210> 13

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Oleosin - Protein A Fusion

<400> 13

Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp
1 5 10 15

Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly

20	25	30
Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr 35 40 45		
Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu 50 55 60		
Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile 65 70 75 80		
Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile 85 90 95		
Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val 100 105 110		
Phe Ser Trp Ile Tyr 115		
<210> 14		
<211> 324		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> Oleosin - Protein A Fusion		
<400> 14		
Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala 1 5 10 15		
Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln 20 25 30		
Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr 35 40 45		
Arg Gly Gly Gln His Thr Thr Leu Val Pro Arg Gly Ser Met Asp Gln 50 55 60		
Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala 65 70 75 80		
Asn Val Leu Gly Glu Ala Gln Lys Leu Asn Asp Ser Gln Ala Pro Lys 85 90 95		
Ala Asp Ala Gln Gln Asn Asn Phe Asn Lys Asp Gln Gln Ser Ala Phe 100 105 110		

Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Ala Gln Arg Asn Gly
115 120 125

Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Thr Asn Val Leu
130 135 140

Gly Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn
145 150 155 160

Asn Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu Asn Met
165 170 175

Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys
180 185 190

Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ser Glu Ala Lys Lys Leu
195 200 205

Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln
210 215 220

Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu
225 230 235 240

Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser
245 250 255

Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro
260 265 270

Lys Ala Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu
275 280 285

Ile Leu His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile
290 295 300

Gln Ser Leu Lys Asp Asp Pro Gly Asn Ser Arg Gly Ser Val Asp Leu
305 310 315 320

Gln Ile Thr Asn